Paurel

1653

> This Raw Listing contains the General Information
> Section and up to first 5 pages.

*Does Not Comply
Corrected Diskette Needed*

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 1   <110> APPLICANT: BURCHELL, BRIAN
 2   <120> TITLE OF INVENTION: DRUG TRIAL ASSAY SYSTEM
 3   <130> FILE REFERENCE: MUR-7450
 4   <140> CURRENT APPLICATION NUMBER: US/09/142,095
 5   <141> CURRENT FILING DATE: 1998-11-02
 6   <150> EARLIER APPLICATION NUMBER: GB 9604480.5
 7   <151> EARLIER FILING DATE: 1996-03-01
 8   <150> EARLIER APPLICATION NUMBER: GB 9605598.3
 9   <151> EARLIER FILING DATE: 1996-03-16
10   <150> EARLIER APPLICATION NUMBER: PCT/GB97/00577
11   <151> EARLIER FILING DATE: 1997-03-03
12   <160> NUMBER OF SEQ ID NOS: 5
13   <170> SOFTWARE: FastSEQ for Windows Version 3.0
14   <210> SEQ ID NO 1
15   <211> LENGTH: 21
16   <212> TYPE: DNA
17   <213> ORGANISM: Artificial Sequence
18   <400> SEQUENCE: 1
19         aagtgaactc cctgctacct t                              21
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21   <211> LENGTH: 21
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23   <213> ORGANISM: Artificial Sequence
24   <400> SEQUENCE: 2
25         ccactgggat caacagtatc t                              21
26   <210> SEQ ID NO 3
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29   <213> ORGANISM: Artificial Sequence
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see item 12 on Error Summary Sheet

RAW SEQUENCE LISTING
PATENT APPLICATION **US/09/142,095**

Input Set: **I142095.RAW**

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45        caagtgagca ggcagtaccg ggggagctgt ggagtgggca ctcttacagg tttccatggc    180
46        gaaagcgggg ggacagttgt gttcttttct ttctaaaagg ctttctaaaa agccttctgt    240
47        ttaatttctg gaaaagaagc ctaacttgtt cactacatag tcgtccttct tcctctctgg    300
48        taacacttgt tggtctgtgg aaatactaat ttaatggatc ctgaggttct ggaagtactt    360
49        tgctgtgttc actcaagaat gtgatttgag tatgaaattc cagccagttc aactgttgtt    420
50        gcctattaag aaacctaata aagctccacc ttctttatct ctgaaagtga actccctgct    480
51        acctttgtgg actgacagct ttttatagtc acgtgacaca gtcaaacatt aacttggtgt    540
52        atcgattggt ttttgccata tatatatata taagtaggag agggcgaacc tctggcagga    600
53        gcaaaggcgc catggctgtg                                                620
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VERIFICATION SUMMARY
PATENT APPLICATION **US/09/142,095**

DATE: 10/26/1999
TIME: 13:13:32

Input Set: **I142095.RAW**

Line ? Error/Warning   Original Text
----- - ------------------------------------ --

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/142,095_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos — The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length — The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering — The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII — This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES) — Sequence(s) _____ are missing this mandatory field or its response.

12 _J_ Use of <220>Feature (NEW RULES) — Sequence(s) _/-S_ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.